

STIC-ILL

ND 432161 (or)

From: Portner, Ginny
Sent: Thursday, February 13, 2003 2:03 PM
To: STIC-ILL
Subject: 09/895,913

Importance: High

00453860 INSIDE CONFERENCE ITEM ID: CN004355891
Molecular Cloning and Nucleotide Sequence Determination of htrA, a Gene
Encoding a 48-kDa Stress Protein of Helicobacter pylori
Kleanthous, H.; Clayton, C. L.; Morgan, D. D.; Pallen, M. J.
CONFERENCE: Basic and clinical aspects of helicobacter pylori infection-
4th Workshop
P: 195-202
New York, Springer-Verlag, c1994
ISBN: 3540567208; 0387567208
LANGUAGE: English DOCUMENT TYPE: Conference Selected papers
CONFERENCE EDITOR(S): Gasbarrini, G.; Pretolani, S.
CONFERENCE SPONSOR: European Helicobacter Pylori Study Group
CONFERENCE LOCATION: Boiogna, Italy
CONFERENCE DATE: Nov 1991 (199111) (199111)

BRITISH LIBRARY ITEM LOCATION: 94/09285 Basic

NOTE:

xii, 313 p.; Described as proceedings. See also 4588.3404 vol 23 no 9
and supp 1 2 1991 for abstracts and programme

DESCRIPTORS: helicobacter pylori infection; helicobacter pylori.

Ginny Portner
CM1, Art Unit 1645
Room 7e13
Mail box 7e12
(703) 308-7543

C1577
2/14

tr	<u>O25663</u>	Serine protease (HTRA) [HP1019] [Helicobacter pylori (...]	834	0.0
tr	<u>Q9ZM18</u>	Protease DO [HTRA] [Helicobacter pylori J99 (Campyloba...	813	0.0
tr	<u>Q9PN69</u>	Serine protease (Protease DO) (EC 3.4.21.-) [HTRA] [Ca...	388	e-107
tr	<u>Q46120</u>	Serine protease [HTRA] [Campylobacter jejuni]	387	e-106
tr	<u>Q46094</u>	Heat shock protein/serine protease (Fragment) [HTRA] [...]	347	2e-94
tr	<u>Q8YHL4</u>	Protease DO (EC 3.4.21.-) [BMEI0783] [Brucella meliten...	291	1e-77
tn	<u>AAN30126</u>	Serine protease [BR1207] [Brucella suis]	291	1e-77
tr	<u>Q44596</u>	HtrA-like protein [Brucella abortus]	289	4e-77
sp	<u>P18584</u>	DEGP_CHLTR Probable serine protease do-like precursor ...	289	5e-77
tr	<u>Q9FD11</u>	HtrA-like serine protease [PRTS1] [Aeromonas hydrophila]	288	7e-77
tn	<u>AAN56917</u>	Serine protease, HtrA/DegQ/DegS family [SO3942] [She...	287	2e-76
tr	<u>Q9KUF5</u>	Protease DO [VC0566] [Vibrio cholerae]	286	3e-76
tr	<u>Q8XV99</u>	Probable HTRA-like serine protease signal peptide prot...	286	3e-76
tn	<u>AAO09118</u>	Protease DO [VV10603] [Vibrio vulnificus]	286	3e-76
sp	<u>Q9PL97</u>	DEGP_CHLMU Probable serine protease do-like precursor ...	285	6e-76
tr	<u>Q8KCH4</u>	Serine protease [CT1447] [Chlorobium tepidum]	285	6e-76
sp	<u>Q9Z6T0</u>	DEGP_CHLPN Probable serine protease do-like precursor ...	282	5e-75
tr	<u>Q8L1C3</u>	DegQ serine protease [Pasteurella piscicida (Photobact...	276	4e-73
tn	<u>BAC24289</u>	DegQ protein [degQ] [Wigglesworthia brevipalpis]	276	5e-73
tn	<u>AAN66925</u>	HtrA-like protease AlgW [algW] [Pseudomonas putida]	275	1e-72
tr	<u>Q57155</u>	MUCD (Serine protease MUCD) [MUCD] [Pseudomonas aerugi...	273	2e-72
tr	<u>Q9ALS1</u>	MucD [MUCD] [Pseudomonas aeruginosa]	273	2e-72
tr	<u>Q8Z9B0</u>	Protease DO, heat shock protein HtrA [STY0231] [Salmon...	272	5e-72
tn	<u>AAN78691</u>	Protease do precursor (EC 3.4.21.-) [htrA] [Escheric...	272	7e-72
sp	<u>P26982</u>	DEGP_SALTY Protease do precursor (EC 3.4.21.-) [DEGP] ...	271	1e-71
tn	<u>BAC50633</u>	Serine protease [bll5368] [Bradyrhizobium japonicum]	271	2e-71
sp	<u>P09376</u>	DEGP_ECOLI Protease do precursor (EC 3.4.21.-) [DEGP] ...	270	2e-71
tn	<u>AAN41816</u>	Periplasmic serine protease Do, heat shock protein H...	268	1e-70
tr	<u>Q98CS8</u>	Serine protease, HtrA/DegQ/DegS family [MLL5022] [Rhiz...	267	2e-70
tr	<u>O67436</u>	Periplasmic serine protease [HTRA] [Aquifex aeolicus]	264	1e-69
tr	<u>Q9LBK0</u>	Heat shock protein HtrA [HTRA] [Shigella sonnei]	264	1e-69
tr	<u>Q9HVX1</u>	AlgW protein [ALGW] [Pseudomonas aeruginosa]	263	2e-69
sp	<u>P45129</u>	HTOA_HAEIN Probable periplasmic serine protease do/hho...	262	5e-69
tr	<u>Q8RSS1</u>	HtrA protein [HTRA] [Klebsiella pneumoniae]	262	5e-69
tr	<u>Q8ZB58</u>	Protease (EC 3.4.21.-) [DEGQ] [Yersinia pestis]	262	7e-69
tn	<u>AAM83731</u>	Serine endoprotease [degQ] [Yersinia pestis]	262	7e-69
tr	<u>Q9AQD1</u>	MucD [MUCD] [Pseudomonas syringae (pv. syringae)]	260	3e-68
tr	<u>Q8UE46</u>	Serine protease [HTRA] [Agrobacterium tumefaciens (str...	259	6e-68
tr	<u>Q8UGQ8</u>	Serine protease DO-like protease [DOP] [Agrobacterium ...]	258	8e-68
tr	<u>O68198</u>	HtrA [Haemophilus influenzae]	257	2e-67
tr	<u>O68197</u>	HTRA (Fragment) [Haemophilus influenzae]	257	2e-67
tr	<u>O31388</u>	DegP protein [DEGP] [Bradyrhizobium japonicum]	256	3e-67
tn	<u>BAC50500</u>	Serine protease [degP] [Bradyrhizobium japonicum]	256	3e-67
sp	<u>Q92JA1</u>	DEGP_RICCN Probable serine protease do-like precursor ...	255	7e-67
tn	<u>AAN67052</u>	Alginate biosynthesis negative regulator, serine pro...	255	7e-67
tr	<u>Q8P418</u>	Protease Do [HTRA] [Xanthomonas campestris (pv. campes...	254	1e-66
tr	<u>Q9CMS7</u>	HtrA [HTRA] [Pasteurella multocida]	254	1e-66
tr	<u>P74978</u>	GsrA protein [GSRA] [Yersinia enterocolitica]	254	1e-66
sp	<u>P39099</u>	DEGQ_ECOLI Protease degQ precursor (EC 3.4.21.-) [DEGQ...	253	2e-66
tr	<u>Q8X9F1</u>	Serine endoprotease [DEGQ] [Escherichia coli O157:H7]	253	2e-66
tr	<u>Q8ZBM6</u>	Global stress requirement protein GsrA [GSRA] [Yersini...	253	2e-66
tn	<u>AAM84394</u>	Periplasmic serine protease Do [htrA] [Yersinia pestis]	253	2e-66
tn	<u>AAN82429</u>	Protease degQ precursor (EC 3.4.21.-) [degQ] [Escher...	253	2e-66
sp	<u>Q44597</u>	DEGP_BRUAB Probable serine protease do-like precursor ...	252	6e-66
tr	<u>Q8PFK1</u>	Protease DO [HTRA] [Xanthomonas axonopodis (pv. citri)]	252	6e-66
tr	<u>Q8YG32</u>	Protease DO (EC 3.4.21.-) [BMEI1330] [Brucella meliten...	252	6e-66
tn	<u>BAC48395</u>	Serine protease DO-like precursor [blr3130] [Bradyrh...	252	7e-66
sp	<u>P57322</u>	DEGP_BUCAI Probable serine protease do-like precursor ...	251	1e-65
tr	<u>Q8UDS7</u>	Serine protease DO-like [HTRA] [Agrobacterium tumefaci...	251	1e-65
tn	<u>AAO26942</u>	Serine protease (EC 3.4.21.-) [htrA] [Buchnera aphid...	251	2e-65
tr	<u>Q8Z3E6</u>	Serine protease (EC 3.4.21.-) [DEGQ] [Salmonella typhi]	248	8e-65
tr	<u>Q98N31</u>	Heat shock protein HtrA like [MLR0328] [Rhizobium loti...	247	2e-64
tr	<u>Q8ZLQ1</u>	Serine endoprotease (EC 3.4.21.-) [DEGQ] [Salmonella t...	247	2e-64
tr	<u>Q9PGL3</u>	Heat shock protein [XF0285] [Xylella fastidiosa]	247	2e-64
tr	<u>Q8KKV0</u>	Hypothetical protein [HTRA] [Rhizobium etli]	247	2e-64

tn	AAO28122	Heat shock protein [htrA] [Xylella fastidiosa Temecu...	247	2e-64
tr	Q8XPT5	Probable protease signal peptide protein (EC 3.4.-.-) ...	246	5e-64
sp	O85291	DEGP_BUCAP Probable serine protease do-like precursor ...	245	7e-64
tn	BAC51771	Serine protease DO-like precursor [bll6506] [Bradyrh...	245	7e-64
tr	Q985F9	Serine protease [MLR7692] [Rhizobium loti (Mesorhizobi...	244	2e-63
tr	Q56885	HtrA protein (Fragment) [HTRA] [Yersinia enterocolitica]	244	2e-63
tn	BAC47856	Serine protease DO-like protease [dop] [Bradyrhizobi...	244	2e-63
tr	Q92QE6	Probable protease protein (EC 3.4.21.-) [DEGP3] [Rhizo...	243	3e-63
tr	Q44652	Immunoreactive stress response protein precursor [Bruc...	240	3e-62
tr	Q98KJ1	Probable serine protease [MLL1451] [Rhizobium loti (Me...	239	5e-62
tr	Q9PBA3	Periplasmic protease [XF2241] [Xylella fastidiosa]	238	8e-62
tn	AAO29135	Periplasmic protease [mucD] [Xylella fastidiosa Teme...	237	2e-61
tr	Q926C8	Putative protease precursor signal peptide protein (EC...	237	2e-61
tr	Q8PB56	Periplasmic protease [MUCD] [Xanthomonas campestris (p...	234	1e-60
tr	Q8PMV4	Periplasmic protease [MUCD] [Xanthomonas axonopodis (p...	234	1e-60
tr	Q8RTK2	Protease MucD [MUCD] [Xanthomonas campestris (pv. camp...	234	1e-60
tn	AAN44738	Serine endoprotease [degQ] [Shigella flexneri]	234	1e-60
sp	O05942	DEGP_RICPR Probable serine protease do-like precursor ...	234	2e-60
sp	P54925	DEGP_BARHE Probable periplasmic serine protease DO-lik...	233	3e-60
sp	Q52894	DEGP_RHIME Probable serine protease do-like precursor ...	232	6e-60
tr	Q8Y0I6	Probable periplasmic protease signal peptide protein (...)	231	1e-59
tr	F73354	Serine protease HTRA [HTRA] [Synechocystis sp. (strain...	231	1e-59
tr	Q9JVT1	Putative periplasmic serine protease (EC 3.4.21.-) [NM...	230	3e-59
tn	AAN48008	Serine protease DO [LA0809] [Leptospira interrogans]	229	4e-59
tr	Q8YI32	Protease DO (EC 3.4.21.-) [BMEI0613] [Brucella meliten...	228	9e-59
tn	AAN30307	Serine protease Do, putative [BR1394] [Brucella suis]	228	9e-59
tr	Q9KJN6	Putative serine protease DO-like [HTRA] [Myxococcus xa...	225	1e-57
tr	Q9A4S2	Serine protease HtrA [CC2758] [Caulobacter crescentus]	223	4e-57
tr	O06439	ORF E0 protein [Rhodobacter capsulatus (Rhodopseudomon...	222	8e-57
tn	BAC08222	Periplasmic serine proteinase [tlr0671] [Synechococc...	219	7e-56
tr	Q9WZ41	Heat shock serine protease, periplasmic [TM0571] [Ther...	218	9e-56
tr	Q51374	AlgW [Pseudomonas aeruginosa]	218	1e-55
tr	Q8YVH0	Serine proteinase [ALL2008] [Anabaena sp. (strain PCC ...	215	1e-54
sp	P44947	DEGS_HAEIN Protease degS precursor (EC 3.4.21.-) [DEGS...	214	2e-54
tr	Q9A8R9	Serine protease [CC1282] [Caulobacter crescentus]	209	7e-53

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Taxonomic view	NiceBlast view	Printable view
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Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software. It is implemented on hardware provided by HP.

In case of problems, please [contact us](#).

NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query length: 443 AA (of which 3% low-complexity regions filtered out)
 Date run: 2003-02-13 14:19:37 UTC+0100 on sib-blast.unil.ch
 Program: NCBI BLASTP 2.2.5 [Nov-16-2002]
 Database: XXtremlnew; XXtreml; XXswissprot
 1,034,081 sequences; 330,203,360 total letters
 Swiss-Prot Release 40.43 of 12-Feb-2003
 TrEMBL Release 22.12 of 07-Feb-2003
 TrEMBL_new of 07-Feb-2003

List of potentially matching sequences

Send selected sequences to [Clustal W \(multiple alignment\)](#)

☐ Include query sequence

Db AC	Description	Score	E-value
<input type="checkbox"/> tr Q25663	Serine protease (HTRA) [HP1019] [Helicobacter pylori (...]	834	0.0
<input type="checkbox"/> tr Q9ZM18	Protease DO [HTRA] [Helicobacter pylori J99 (Campyloba...	813	0.0
<input type="checkbox"/> tr Q9PN69	Serine protease (Protease DO) (EC 3.4.21.-) [HTRA] [Ca...	388	e-107
<input type="checkbox"/> tr Q46120	Serine protease [HTRA] [Campylobacter jejuni]	387	e-106
<input type="checkbox"/> tr Q46094	Heat shock protein/serine protease (Fragment) [HTRA] [...]	347	2e-94
<input type="checkbox"/> tr Q8YHL4	Protease DO (EC 3.4.21.-) [BMEI0783] [Brucella meliten...	291	1e-77
<input type="checkbox"/> tn AAN30126	Serine protease [BR1207] [Brucella suis]	291	1e-77

<input type="checkbox"/>	tr	Q44596	HtrA-like protein [Brucella abortus]	289	4e-77
<input type="checkbox"/>	sp	P18584	DEGP_CHLTR Probable serine protease do-like precursor ...	289	5e-77
<input type="checkbox"/>	tr	Q9FD11	HtrA-like serine protease [PRTS1] [Aeromonas hydrophila]	288	7e-77
<input type="checkbox"/>	tn	AAN56917	Serine protease, HtrA/DegQ/DegS family [SO3942] [She...]	287	2e-76
<input type="checkbox"/>	tr	Q9KUF5	Protease DO [VC0566] [Vibrio cholerae]	286	3e-76
<input type="checkbox"/>	tr	Q8XV99	Probable HTRA-like serine protease signal peptide prot...	286	3e-76
<input type="checkbox"/>	tn	AAO09118	Protease DO [VV10603] [Vibrio vulnificus]	286	3e-76
<input type="checkbox"/>	sp	Q9PL97	DEGP_CHLMU Probable serine protease do-like precursor ...	285	6e-76
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<input type="checkbox"/>	tr	Q8L1C3	DegQ serine protease [Pasteurella piscicida (Photobact...]	276	4e-73
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<input type="checkbox"/>	tr	Q57155	MUCD (Serine protease MUCD) [MUCD] [Pseudomonas aerugi...]	273	2e-72
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<input type="checkbox"/>	sp	P26982	DEGP_SALTY Protease do precursor (EC 3.4.21.-) [DEGP] ...	271	1e-71
<input type="checkbox"/>	tn	BAC50633	Serine protease [bll5368] [Bradyrhizobium japonicum]	271	2e-71
<input type="checkbox"/>	sp	P09376	DEGP_ECOLI Protease do precursor (EC 3.4.21.-) [DEGP] ...	270	2e-71
<input type="checkbox"/>	tn	AAN41816	Periplasmic serine protease Do, heat shock protein H...	268	1e-70
<input type="checkbox"/>	tr	Q98CS8	Serine protease, HtrA/DegQ/DegS family [MLL5022] [Rhiz...]	267	2e-70
<input type="checkbox"/>	tr	O67436	Periplasmic serine protease [HTRA] [Aquifex aeolicus]	264	1e-69
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<input type="checkbox"/>	sp	P45129	HTOA_HAEIN Probable periplasmic serine protease do/hho...	262	5e-69
<input type="checkbox"/>	tr	Q8RSS1	HtrA protein [HTRA] [Klebsiella pneumoniae]	262	5e-69
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<input type="checkbox"/>	tr	O68198	HtrA [Haemophilus influenzae]	257	2e-67
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<input type="checkbox"/>	sp	Q92JA1	DEGP_RICCN Probable serine protease do-like precursor ...	255	7e-67
<input type="checkbox"/>	tn	AAN67052	Alginate biosynthesis negative regulator, serine pro...	255	7e-67
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<input type="checkbox"/>	tr	Q9CMS7	HtrA [HTRA] [Pasteurella multocida]	254	1e-66
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<input type="checkbox"/>	tr	Q8ZBM6	Global stress requirement protein GsrA [GSRA] [Yersini...]	253	2e-66
<input type="checkbox"/>	tn	AAM84394	Periplasmic serine protease Do [htrA] [Yersinia pestis]	253	2e-66

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<input type="checkbox"/>	tr	Q8PFK1	Protease DO [HTRA] [Xanthomonas axonopodis (pv. citri)]	252	6e-66
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<input type="checkbox"/>	tr	Q8UDS7	Serine protease DO-like [HTRA] [Agrobacterium tumefaci...	251	1e-65
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<input type="checkbox"/>	tr	Q8Z3E6	Serine protease (EC 3.4.21.-) [DEGQ] [Salmonella typhi]	248	8e-65
<input type="checkbox"/>	tr	Q98N31	Heat shock protein HtrA like [MLR0328] [Rhizobium loti...	247	2e-64
<input type="checkbox"/>	tr	Q8ZLQ1	Serine endoprotease (EC 3.4.21.-) [DEGQ] [Salmonella t...	247	2e-64
<input type="checkbox"/>	tr	Q9PGL3	Heat shock protein [XF0285] [Xylella fastidiosa]	247	2e-64
<input type="checkbox"/>	tr	Q8KKV0	Hypothetical protein [HTRA] [Rhizobium etli]	247	2e-64
<input type="checkbox"/>	tn	AAO28122	Heat shock protein [htrA] [Xylella fastidiosa Temecu...	247	2e-64
<input type="checkbox"/>	tr	Q8XPT5	Probable protease signal peptide protein (EC 3.4.-.-) ...	246	5e-64
<input type="checkbox"/>	sp	O85291	DEGP_BUCAP Probable serine protease do-like precursor ...	245	7e-64
<input type="checkbox"/>	tn	BAC51771	Serine protease DO-like precursor [bll6506] [Bradyrh...	245	7e-64
<input type="checkbox"/>	tr	Q985F9	Serine protease [MLR7692] [Rhizobium loti (Mesorhizobi...	244	2e-63
<input type="checkbox"/>	tr	Q56885	HtrA protein (Fragment) [HTRA] [Yersinia enterocolitica]	244	2e-63
<input type="checkbox"/>	tn	BAC47856	Serine protease DO-like protease [dop] [Bradyrhizobi...	244	2e-63
<input type="checkbox"/>	tr	Q92QE6	Probable protease protein (EC 3.4.21.-) [DEGP3] [Rhizo...	243	3e-63
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<input type="checkbox"/>	tn	AAO29135	Periplasmic protease [mucD] [Xylella fastidiosa Teme...	237	2e-61
<input type="checkbox"/>	tr	Q926C8	Putative protease precursor signal peptide protein (EC...	237	2e-61
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<input type="checkbox"/>	sp	P54925	DEGP_BARHE Probable periplasmic serine protease DO-lik...	233	3e-60
<input type="checkbox"/>	sp	Q52894	DEGP_RHIME Probable serine protease do-like precursor ...	232	6e-60
<input type="checkbox"/>	tr	Q8Y0I6	Probable periplasmic protease signal peptide protein (...	231	1e-59
<input type="checkbox"/>	tr	P73354	Serine protease HTRA [HTRA] [Synechocystis sp. (strain...	231	1e-59
<input type="checkbox"/>	tr	Q9JVT1	Putative periplasmic serine protease (EC 3.4.21.-) [NM...	230	3e-59
<input type="checkbox"/>	tn	AAN48008	Serine protease DO [LA0809] [Leptospira interrogans]	229	4e-59
<input type="checkbox"/>	tr	Q8YI32	Protease DO (EC 3.4.21.-) [BMEI0613] [Brucella meliten...	228	9e-59
<input type="checkbox"/>	tn	AAN30307	Serine protease Do, putative [BR1394] [Brucella suis]	228	9e-59
<input type="checkbox"/>	tr	Q9KJN6	Putative serine protease DO-like [HTRA] [Myxococcus xa...	225	1e-57
<input type="checkbox"/>	tr	Q9A4S2	Serine protease HtrA [CC2758] [Caulobacter crescentus]	223	4e-57
<input type="checkbox"/>	tr	O06439	ORF E0 protein [Rhodobacter capsulatus (Rhodopseudomon...	222	8e-57
<input type="checkbox"/>	tn	BAC08222	Periplasmic serine proteinase [tlr0671] [Synechococc...	219	7e-56
<input type="checkbox"/>	tr	Q9WZ41	Heat shock serine protease, periplasmic [TM0571] [Ther...	218	9e-56
<input type="checkbox"/>	tr	Q51374	AlgW [Pseudomonas aeruginosa]	218	1e-55

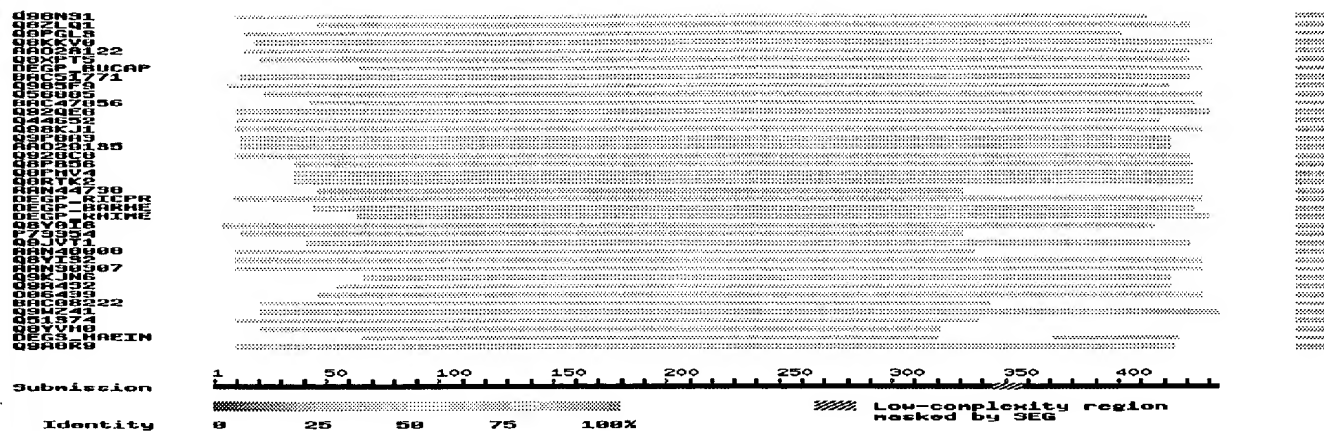
<input type="checkbox"/>	tr Q8YVH0	Serine proteinase [ALL2008] [Anabaena sp. (strain PCC ...	215	1e-54
<input type="checkbox"/>	sp P44947	DEGS_HAEIN Protease degS precursor (EC 3.4.21.-) [DEGS...	214	2e-54
<input type="checkbox"/>	tr Q9A8R9	Serine protease [CC1282] [Caulobacter crescentus]	209	7e-53

Graphical overview of the alignments

[Click here](#)to resubmit your query after masking regions matching [PROSITE](#) profiles or [Pfam](#) HMMs

new

(use [ScanProsite](#) for more details about PROSITE matches)



Alignments

tr 025663 **Serine protease (HTRA) [HP1019] [Helicobacter pylori** 443 AA
(**Campylobacter**
pylori] align

Score = 834 bits (2154), Expect = 0.0
Identities = 430/443 (97%), Positives = 430/443 (97%)

Query: 1 MSPLKTIRIYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGVFNDPFFQQFFGDLGGMIPK 60
MSPLKTIRIYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGVFNDPFFQQFFGDLGGMIPK
Sbjct: 1 MSPLKTIRIYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGVFNDPFFQQFFGDLGGMIPK 60

Query: 61 ERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIR 120
ERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIR
Sbjct: 61 ERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIR 120

Query: 121 ITKDNLPITIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQT 180
ITKDNLPITIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQT
Sbjct: 121 ITKDNLPITIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQT 180

Query: 181 DASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDVTVQLIKTGKIE 240
DASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDVTVQLIKTGKIE
Sbjct: 181 DASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDVTVQLIKTGKIE 240

Query: 241 RGYLGVLQDLQNSYDNKEGAVVISVEKDSPAAGILVWDLITEVNGKKVKNTNE 300
RGYLGVLQDLQNSYDNKEGAVVISVEKDSPAAGILVWDLITEVNGKKVKNTNE
Sbjct: 241 RGYLGVLQDLQNSYDNKEGAVVISVEKDSPAAGILVWDLITEVNGKKVKNTNE 300

Query: 301 LRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISXXXXXXXXXXXXXVED 360
LRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETIS VED
Sbjct: 301 LRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQQQLNGLQVED 360

Query: 361 LTQETKRSMRLSDDVQGVVLSQVNENSPAEGAGFRQGNIIITKIEEVEVKSVADFNHALEK 420
LTQETKRSMRLSDDVQGVVLSQVNENSPAEGAGFRQGNIIITKIEEVEVKSVADFNHALEK
Sbjct: 361 LTQETKRSMRLSDDVQGVVLSQVNENSPAEGAGFRQGNIIITKIEEVEVKSVADFNHALEK 420

Query: 421 YKGKPKRFLVLDLNQGYRIILVK 443
YKGKPKRFLVLDLNQGYRIILVK
Sbjct: 421 YKGKPKRFLVLDLNQGYRIILVK 443

tr Q9ZM18 **Protease DO [HTRA] [Helicobacter pylori J99 (Campylobacter pylori J99)]** 476 AA
align

Score = 813 bits (2099), Expect = 0.0
Identities = 420/441 (95%), Positives = 421/441 (95%)

Query: 3 PLKTIRIYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGVFNDPFFQQFFGDLGGMIPKER 62
P K IYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGVFNDPFFQQFFGDLGGMIPKER
Sbjct: 36 PSKEDTIYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGVFNDPFFQQFFGDLGGMIPKER 95

Query: 63 MERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRIT 122
MERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRIT
Sbjct: 96 MERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRIT 155

Query: 123 KDNLPSTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSIGIGINSYENFIQTDA 182
KDNLPSTIKFSDSNDI VGDLVFAIGNPFGVGESVTQGIVSALNKSIGIGINSYENFIQTDA
Sbjct: 156 KDNLPSTIKFSDSNDILVGDLVFAIGNPFGVGESVTQGIVSALNKSIGIGINSYENFIQTDA 215

Query: 183 SINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDVTQLIKTGKIERG 242
SINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKD VTQLIKTGKIERG
Sbjct: 216 SINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDIVTQLIKTGKIERG 275

Query: 243 YLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAAGILVWDLITEVNGKKVKNTNELR 302
YLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAAGILVWDLITEVNGKKVKNTNELR
Sbjct: 276 YLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAAGILVWDLITEVNGKKVKNTNELR 335

Query: 303 NLIGSMLPNQRVTLKVIRDKKERAFITLTLAERKNPNKKETISXXXXXXXXXXXXVEDLT 362
NLIGSMLPNQRVTLKVIRDKKER FTTLAERKNPNKKETIS VEDLT
Sbjct: 336 NLIGSMLPNQRVTLKVIRDKKERTFTTLAERKNPNKKETISAQNGVQGQLNGLQVEDLT 395

Query: 363 QETKRSMRLSDDVQGVVLSQVNENSPAEGAGFRQGNIIITKIEEVEVKSVADFNHALEKYK 422
Q+TKRSMRLSDDVQGVVLSQVNENSPAEGAGFRQGNIIITKIEEVEVKSVADFNHALEKYK
Sbjct: 396 QETKRSMRLSDDVQGVVLSQVNENSPAEGAGFRQGNIIITKIEEVEVKSVADFNHALEKYK 455

Query: 423 GKPKRFLVLDLNQGYRIILVK 443
GKPKRFLVLDLNQGYRIILVK
Sbjct: 456 GKPKRFLVLDLNQGYRIILVK 476

tr Q9PN69 **Serine protease (Protease DO) (EC 3.4.21.-) [HTRA]** 472 AA
[**Campylobacter**
jejuni] align

Score = 388 bits (996), Expect = e-107

Identities = 212/431 (49%), Positives = 291/431 (67%), Gaps = 15/431 (3%)

Query: 1 MSPLKTIRIYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGV---FNDPFFQQFFG-DLGG 56
++P + SYHDSIKD+ K+VVNIST K I + FNDP+F+QFF D
Sbjct: 31 VNPAAGNAVLSYHDSIKDAKKS VVNISTSKTITRANRPSPLDDFFNDPYFKQFFDFDFSQ 90

Query: 57 MIPKERME--RALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSES 114
K E +LGSGVIISKDGYIVTNNHV+D AD I V +PGS+ EY A L+G D ++
Sbjct: 91 RKGKNDKEVVSSLGSGVIISKDGYIVTNNHVVDADTITVNLPGSDIEYKAKLIGKDPKT 150

Query: 115 DLAVIRITKDNLPITIKFSDSNDISVGD LVFAIGNPFGVGESVTQGIVSALNKSGIGINSY 174
DLAVI+I +NL I F++S+D+ GD+VFA+GNPFGVG SVT GI+SALNK IG+N Y
Sbjct: 151 DLAVIKIEANNLSAITFTNSDDLMEGDVVFALGNPFGVGSVTSGIISALNKDNIGLNQY 210

Query: 175 ENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGNGHIGGFAIPSNMVKDTVTQLI 234
ENFIQTDASINPGNSGGAL+DSRG LVGIN+AI+S+ GGN+GIGFAIPSNMVKD +LI
Sbjct: 211 ENFIQTDASINPGNSGGALVDSRGYLVGINSAILSRGGNGGIGFAIPSNMVKDI AKKLI 270

Query: 235 KTGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKK 294
+ GKI+RG+LGV + L GD + +Y N+EGA++ V+K S A +AG+ DL+T+VN K
Sbjct: 271 EKGKIDRGFLGV TILALQGD TTKAYKNQEGALITDVQKGSSADEAGLKRGD LVTKVNDKV 330

Query: 295 VKNTNELRNLI G SMLPNQRVTLKVIRD-KKERAFTLT LAERKNPNKKETISXXXXXXXXXX 353
+K+ +L+N IG++ Q+++L RD + ++A + E++NP ++
Sbjct: 331 IKSPIDLKNYIGTLEIGQKISLSYERDGENKQASFILKGEKENPKGVQS-----DLI 382

Query: 354 XXXXVEDLTQETKRSMRLSDDVQGV LVSVQVNENSPA EQAGFRQGNII TKIEEVEVKSVAD 413
+ +L K +++ DV GVLV V E S + +GF++G+II + + E+K++ D
Sbjct: 383 DGLSLRNLDPRLKDR LQIPKDVNGVLVDSVKEKSKGKNSGFQEGDIIIGVGQSEIKNLKD 442

Query: 414 FNHALEKYKGK 424
AL++ K
Sbjct: 443 LEQALKQVNKK 453

SYSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1966-2003/Feb W2

(c) format only 2003 The Dialog Corp.

File 349:PCT FULLTEXT 1979-2002/UB=20030206,20030123

(c) 2003 WIPO/Univentio

File 5:Biosis Previews(R) 1969-2003/Feb W2

(c) 2003 BIOSIS

*File 5: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 449:IMS Company Profiles 1992-2003/Mar

(c) 2003 IMS Health & Affiliates

File 34:SciSearch(R) Cited Ref Sci 1990-2003/Feb W2

(c) 2003 Inst for Sci Info

*File 34: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 71:ELSEVIER BIOBASE 1994-2003/Feb W2

(c) 2003 Elsevier Science B.V.

File 73:EMBASE 1974-2003/Feb W1

(c) 2003 Elsevier Science B.V.

*File 73: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 440:Current Contents Search(R) 1990-2003/Feb 13

(c) 2003 Inst for Sci Info

*File 440: Daily alerts are now available.

File 65:Inside Conferences 1993-2003/Feb W2

(c) 2003 BLDSC all rts. reserv.

File 636:Gale Group Newsletter DB(TM) 1987-2003/Feb 12

(c) 2003 The Gale Group

File 144:Pascal 1973-2003/Feb W1

(c) 2003 INIST/CNRS

File 399:CA SEARCH(R) 1967-2003/UD=13807

(c) 2003 American Chemical Society

*File 399: Use is subject to the terms of your user/customer agreement. Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description

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Cost is in DialUnits

?ds

Set Items Description

S1 25 HTRA (10N) (PYLROI OR PYLORI OR PYLORIS OR PYLORIDIS OR PYLORUM OR HPYLORI? OR HELICOBACTER?)

S2 15 RD (unique items)

?t s2/9/13

2/9/13 (Item 1 from file: 65)

DIALOG(R)File 65:Inside Conferences

(c) 2003 BLDSC all rts. reserv. All rts. reserv.

00453860 INSIDE CONFERENCE ITEM ID: CN004355891

Molecular Cloning and Nucleotide Sequence Determination of htrA , a Gene Encoding a 48-kDa Stress Protein of Helicobacter pylori

Kleanthous, H.; Clayton, C. L.; Morgan, D. D.; Pallen, M. J.

CONFERENCE: Basic and clinical aspects of helicobacter pylori infection-4th Workshop

P: 195-202

New York, Springer-Verlag, c1994

ISBN: 3540567208; 0387567208

LANGUAGE: English DOCUMENT TYPE: Conference Selected papers

CONFERENCE EDITOR(S): Gasbarrini, G.; Pretolani, S.

CONFERENCE SPONSOR: European Helicobacter Pylori Study Group

CONFERENCE LOCATION: Bologna, Italy

CONFERENCE DATE: Nov 1991 (199111) (199111)

BRITISH LIBRARY ITEM LOCATION: 94/09285 Basic

NOTE:

xii, 313 p.; Described as proceedings. See also 4588.3404 vol 23 no 9
and supp 1 2 1991 for abstracts and programme

DESCRIPTORS: helicobacter pylori infection; helicobacter pylori

?t s2/3,kwic/3-7 9-11

>>>KWIC option is not available in file(s): 399

WEST Search History

DATE: Thursday, February 13, 2003

Set Name Query

side by side

Hit Count Set Name

result set

DB=USPT; PLUR=YES; OP=AND

L1	pox\$.clm.	391	L1
L2	L1 same (htra or htr-a or proteinase or protease or peptidase)	4	L2
L3	L1 same (htra or htr-a or proteinase or protease or peptidase).clm.	4	L3
L4	poxv\$.clm.	142	L4
L5	L4 same (htra or htr-a or proteinase or protease or peptidase).clm.	1	L5
L6	L4 and (htra or htr-a or proteinase or protease or peptidase).clm.	2	L6
L7	L4 and (serine).clm.	1	L7
L8	poxv\$ same (htra or htr-a or proteinase or protease or peptidase)	40	L8
L9	L8 not l3 not l6	39	L9
L10	L9 same (htr or serine)	3	L10
L11	L9 same (htra or htr-a or serine)	3	L11

END OF SEARCH HISTORY